

# SCORE Search Results Details for Application 10751113 and Search Result us-10-751-113-3.rge.

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 25, 2006, 13:42:05 ; Search time 1996 Seconds  
(without alignments)  
1601.889 Million cell updates/sec

Title: US-10-751-113-3  
Perfect score: 50  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
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5: gb\_pr:\*  
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7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27.8	55.6	480	2	CQ712958	CQ712958 Sequence
2	27.8	55.6	4495	2	CS162240	CS162240 Sequence

3	27.8	55.6	4495	5	AF010227	AF010227 Homo sapi
4	27.8	55.6	4668	5	AF016031	AF016031 Homo sapi
5	27.8	55.6	4807	5	BC092516	BC092516 Homo sapi
6	27.8	55.6	5256	5	AB209863	AB209863 Homo sapi
7	27.8	55.6	6754	2	CS032155	CS032155 Sequence
8	27.8	55.6	6754	2	CS032413	CS032413 Sequence
9	27.8	55.6	6754	2	CS032417	CS032417 Sequence
10	27.8	55.6	6754	2	CS041107	CS041107 Sequence
11	27.8	55.6	6754	2	CS041365	CS041365 Sequence
12	27.8	55.6	6754	2	CS041369	CS041369 Sequence
13	27.8	55.6	6754	2	CS050236	CS050236 Sequence
14	27.8	55.6	6754	2	AX821998	AX821998 Sequence
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## ALIGNMENTS

## RESULT 1

CQ712958

LOCUS CQ712958 480 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 57884 from Patent WO02070737.

ACCESSION CQ712958

VERSION CQ712958.1 GI:42273815

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1

AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.

TITLE Compositions and methods relating to osteoarthritis

JOURNAL Patent: WO 02070737-A 57884 12-SEP-2002;

Chondrogene Inc. (CA)

FEATURES

Location/Qualifiers

source

1..480

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ORIGIN

Query Match 55.6%; Score 27.8; DB 2; Length 480;

Best Local Similarity 82.1%; Pred. No. 14;

Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 396 AATAAAGAGCAAGGAAAACTATTTC CAATGATGATGA 434

## RESULT 2

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CS162240
LOCUS          CS162240                4495 bp    DNA        linear    PAT 21-SEP-2005
DEFINITION     Sequence 481 from Patent WO2005083429.
ACCESSION      CS162240
VERSION        CS162240.1  GI:76060367
KEYWORDS       .
SOURCE         Homo sapiens (human)
               ORGANISM  Homo sapiens
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                   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                   Hominidae; Homo.
REFERENCE      1
AUTHORS        Wang, Y.
TITLE          Breast cancer prognostics
JOURNAL        Patent: WO 2005083429-A 481 09-SEP-2005;
               Veridex, LLC (US)
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Db 328 AATAAAGAGCAAGGGA AAAACTATTTCCAATGATGATGA 366

### RESULT 3

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AF010227
LOCUS      AF010227                4495 bp    mRNA    linear    PRI 13-AUG-1997
DEFINITION Homo sapiens receptor-associated coactivator 3 (RAC3) mRNA,
            complete cds.
ACCESSION  AF010227
VERSION    AF010227.1  GI:2318005
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 4495)
AUTHORS    Li,H., Gomes,P.J. and Chen,J.D.
TITLE      RAC3, a steroid/nuclear receptor-associated coactivator that is
            related to SRC-1 and TIF2
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 94 (16), 8479-8484 (1997)
PUBMED      9238002
REFERENCE   2  (bases 1 to 4495)
AUTHORS    Chen,J.D., Li,H. and Gomes,P.J.
TITLE      Direct Submission
JOURNAL     Submitted (25-JUN-1997) Pharmacology and Molecular Toxicology,
            University of Massachusetts Medical School, 55 Lake Avenue North,
            Worcester, MA 01655-0126, USA
FEATURES             Location/Qualifiers
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     CDS              86. .4339
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                     /note="transcriptional coactivator with intrinsic
                     >histone acetyltransferase activity; member of the
                     steroid/nuclear receptor-associated coactivator family

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which includes steroid receptor coactivator 1 (SRC-1), transcriptional intermediate factor 2 (TIF2), and receptor associated coactivator 3; similar to the mouse p300/CBP/co-integrator protein (p/CIP) and the activator of retinoid receptors (ACTR)"

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## ORIGIN

Query Match 55.6%; Score 27.8; DB 5; Length 4495;  
Best Local Similarity 82.1%; Pred. No. 14;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy            12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA    50  
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Db          328 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA    366

#### RESULT 4

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AF016031
LOCUS      AF016031                4668 bp    mRNA    linear    PRI 05-NOV-1997
DEFINITION Homo sapiens thyroid hormone receptor activator molecule (TRAM-1)
            mRNA, complete cds.
ACCESSION  AF016031
VERSION    AF016031.1  GI:2584879
KEYWORDS
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1  (bases 1 to 4668)
  AUTHORS  Takeshita,A., Cardona,G.R., Koibuchi,N., Suen,C.S. and Chin,W.W.
  TITLE    TRAM-1, A novel 160-kDa thyroid hormone receptor activator
            molecule, exhibits distinct properties from steroid receptor
            coactivator-1
            J. Biol. Chem. 272 (44), 27629-27634 (1997)
  JOURNAL  PUBMED
            9346901
REFERENCE  2  (bases 1 to 4668)
  AUTHORS  Takeshita,A., Cardona,G.R., Koibuchi,N. and Chin,W.W.
  TITLE    Direct Submission
  JOURNAL  Submitted (24-JUL-1997) Medicine, Brigham and Women's Hospital,
            Harvard Medical School, 20 Shattuck Street #905, Boston, MA 02115,
            USA
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ORIGIN

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BC092516

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SCHNERCH,A., SCHEIN,J.E., JONES,S.J. and MARRA,M.A.  
 MAMMALIAN GENE COLLECTION PROGRAM TEAM  
 GENERATION AND INITIAL ANALYSIS OF MORE THAN 15,000 FULL-LENGTH  
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 PROC. NATL. ACAD. SCI. U.S.A. 99 (26), 16899-16903 (2002)  
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 2 (bases 1 to 4807)  
 NIH MGC PROJECT  
 DIRECT SUBMISSION  
 SUBMITTED (04-APR-2005) NATIONAL INSTITUTES OF HEALTH, MAMMALIAN  
 GENE COLLECTION (MGC), BETHESDA, MD 20892-2590, USA  
 NIH-MGC PROJECT URL: <http://mgc.nci.nih.gov>  
 CONTACT: MGC HELP DESK  
 EMAIL: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 TISSUE PROCUREMENT: LOUIS M. STAUDT, M.D., Ph.D.  
 cDNA LIBRARY PREPARATION: M. BENTO SOARES, UNIVERSITY OF IOWA  
 cDNA LIBRARY ARRAYED BY: THE I.M.A.G.E. CONSORTIUM (LLNL)  
 DNA SEQUENCING BY: SEQUENCING GROUP AT THE STANFORD HUMAN GENOME  
 CENTER, STANFORD UNIVERSITY SCHOOL OF MEDICINE, STANFORD, CA 94305  
 WEB SITE: <http://www-shgc.stanford.edu>  
 CONTACT: (DICKSON, MARK) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 DICKSON, M., SCHMUTZ, J., GRIMWOOD, J., RODRIGUEZ, A., and MYERS,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
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 Series: IRAK Plate: 199 Row: b Column: 20  
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ORIGIN

Query Match 55.6%; Score 27.8; DB 5; Length 4807;  
Best Local Similarity 82.1%; Pred. No. 14;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy            12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA    50  
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## RESULT 6

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AB209863
LOCUS AB209863 5256 bp mRNA linear PRI 31-MAR-2005
DEFINITION Homo sapiens mRNA for nuclear receptor coactivator 3 isoform a
variant protein.
ACCESSION AB209863
VERSION AB209863.1 GI:62089311
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A., Yokoyama,S.,
Ohara,O., Nagase,T. and F.Kikuno,R.
TITLE None Title
JOURNAL Published Only in Database (2005)
REFERENCE 2 (bases 1 to 5256)
AUTHORS Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A., Yokoyama,S.,
Ohara,O., Nagase,T. and F.Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba, 292-0818, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://protein.gsc.riken.go.jp/, Tel:81-438-52-3930,
Fax:81-438-52-3931)
COMMENT This work was supported in part by the National Project on Protein
Structural and Functional Analysis , Ministry of Education, Culture
, Sports, Science and Technology of Japan. Totoki Y, Toyoda A,
Takeda T, Sakaki Y, Tanaka A, Yokoyama S. RIKEN Genomic Sciences
Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan.
e-mail: aktanaka@postman.riken.go.jp
URL: http://protein.gsc.riken.go.jp/.
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## ORIGIN

## REFERENCE



AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.  
 TITLE Compositions and methods for the treatment of immune related diseases  
 JOURNAL Patent: WO 2005016962-A 1919 24-FEB-2005; Genentech, Inc. (US)  
 FEATURES Location/Qualifiers  
     source 1. .6754  
             /organism="Homo sapiens"  
             /mol\_type="unassigned DNA"  
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## ORIGIN

Query Match 55.6%; Score 27.8; DB 2; Length 6754;  
 Best Local Similarity 82.1%; Pred. No. 14;  
 Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50  
     | | | | | | | | | | | | | | | | | | | | | |  
 Db 426 AATAAAAGAGCAAGGGAAAACTATTTCCAATGATGATGA 464

## RESULT 9

CS032417  
 LOCUS CS032417 6754 bp DNA linear PAT 10-MAR-2005  
 DEFINITION Sequence 1923 from Patent WO2005016962.  
 ACCESSION CS032417  
 VERSION CS032417.1 GI:60731970  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
     ORGANISM Homo sapiens  
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
             Hominidae; Homo.  
 REFERENCE 1  
     AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.  
     TITLE Compositions and methods for the treatment of immune related diseases  
     JOURNAL Patent: WO 2005016962-A 1923 24-FEB-2005; Genentech, Inc. (US)  
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     source 1. .6754  
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             /mol\_type="unassigned DNA"  
             /db\_xref="taxon:9606"

## ORIGIN

Query Match 55.6%; Score 27.8; DB 2; Length 6754;  
 Best Local Similarity 82.1%; Pred. No. 14;  
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 Db 426 AATAAAAGAGCAAGGGAAAACTATTTCCAATGATGATGA 464

## RESULT 10

CS041107  
 LOCUS CS041107 6754 bp DNA linear PAT 22-MAR-2005  
 DEFINITION Sequence 1661 from Patent WO2005019258.  
 ACCESSION CS041107  
 VERSION CS041107.1 GI:61848654  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
     ORGANISM Homo sapiens  
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
             Hominidae; Homo.  
 REFERENCE 1  
     AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.  
     TITLE Compositions and methods for the treatment of immune related diseases  
     JOURNAL Patent: WO 2005019258-A 1661 03-MAR-2005; Genentech, Inc. (US)  
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     source 1. .6754  
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Best Local Similarity 82.1%; Pred. No. 14;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50  
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RESULT 11

CS041365  
LOCUS CS041365 6754 bp DNA linear PAT 22-MAR-2005  
DEFINITION Sequence 1919 from Patent WO2005019258.  
ACCESSION CS041365  
VERSION CS041365.1 GI:61848857  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 2005019258-A 1919 03-MAR-2005;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
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ORIGIN

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Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50  
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Db 426 AATAAAGAGCAAGGGAAAACTATTTCCAATGATGATGA 464

RESULT 12

CS041369  
LOCUS CS041369 6754 bp DNA linear PAT 22-MAR-2005  
DEFINITION Sequence 1923 from Patent WO2005019258.  
ACCESSION CS041369  
VERSION CS041369.1 GI:61848859  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 2005019258-A 1923 03-MAR-2005;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1. .6754  
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ORIGIN

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Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db          426 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA    464

RESULT 13

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CS050236
LOCUS          CS050236                6754 bp    DNA        linear    PAT 23-MAR-2005
DEFINITION     Sequence 20 from Patent WO2005021757.
ACCESSION      CS050236
VERSION        CS050236.1  GI:61889491
KEYWORDS       .
SOURCE         Homo sapiens (human)
   ORGANISM    Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1
   AUTHORS     Tomme,P.H. and van Rompaey,L.
   TITLE       Polypeptides and polynucleotides for use as a medicament
   JOURNAL     Patent: WO 2005021757-A 20 10-MAR-2005;
               Galapagos Genomics N.V. (BE)
FEATURES       Location/Qualifiers
   source      1. .6754
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

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## ORIGIN

Query Match 55.6%; Score 27.8; DB 2; Length 6754;  
Best Local Similarity 82.1%; Pred. No. 14;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy            12 ACTCCAGGACAAGGGAAAACTATTTC CAATGATGATGA 50  
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Db           426 AATAAAAGAGCAAGGAAAACTATTTC CAATGATGATGA 464

RESULT 14

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AX821998
LOCUS      AX821998                      6754 bp    DNA        linear    PAT 10-DEC-2003
DEFINITION Sequence 126 from Patent WO03068961.
ACCESSION  AX821998
VERSION    AX821998.1  GI:39725219
KEYWORDS   .
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
  AUTHORS  Andrews,P.A., Walsh,J.A. and Gokhale,P.A.
  TITLE    Method to modify differentiation of pluripotential stem cells
  JOURNAL  Patent: WO 03068961-A 126 21-AUG-2003;
            Axordia Limited (GB)
FEATURES   Location/Qualifiers
  source   1..6754
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
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ORIGIN

Query Match 55.6%; Score 27.8; DB 2; Length 6754;  
Best Local Similarity 82.1%; Pred. No. 14;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy            12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA    50  
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Db          426 AATAAAGAGCAAGGGAAAACTATTTCCAATGATGATGA    464

RESULT 15

AF036892  
LOCUS AF036892 6754 bp mRNA linear PRI 21-DEC-1997  
DEFINITION Homo sapiens nuclear receptor coactivator (ACTR) mRNA, complete cds.



Search completed: July 25, 2006, 14:15:31  
Job time : 1998 secs

SCORE 1.3 BuildDate: 12/06/2005
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http://es/ScoreAccessWeb/GetItem.action?AppId=10751113&seqId=569424&ItemName=... 8/11/2006

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	38	22.2	44.4	1746	3	US-09-430-806A-5	Sequence 5, Appli
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	42	22.2	44.4	2607	2	US-08-820-754-5	Sequence 5, Appli
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## ALIGNMENTS

## RESULT 1

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US-09-949-016-4981
; Sequence 4981, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4981
; LENGTH: 6760
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4981

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Query Match 55.6%; Score 27.8; DB 3; Length 6760;  
Best Local Similarity 82.1%; Pred. No. 0.93;  
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Db          424 AATAAAGAGCAAGGAAAACTATTTTCCAATGATGATGA    462

## RESULT 2

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US-09-125-635-1
; Sequence 1, Application US/09125635
; Patent No. 6562589
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6835
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(4463)
US-09-125-635-1

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Query Match 55.6%; Score 27.8; DB 3; Length 6835;  
Best Local Similarity 82.1%; Pred. No. 0.93;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db           443 AATAAAGAGCAAGGAAAACTATTTC CAATGATGATGA     481

### RESULT 3

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US-09-949-016-16723
; Sequence 16723, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16723
; LENGTH: 157822
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16723

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Query Match 52.8%; Score 26.4; DB 3; Length 157822;  
Best Local Similarity 96.4%; Pred. No. 6.8;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 122387 TGCCATGTGATACTCCAGGACAAGGGTA 122414

#### RESULT 4

US-09-125-635-9  
; Sequence 9, Application US/09125635  
; Patent No. 6562589  
; GENERAL INFORMATION:  
; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE  
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator  
; FILE REFERENCE: 49944  
; CURRENT APPLICATION NUMBER: US/09/125,635



; CURRENT FILING DATE: 1998-08-21  
; PRIOR APPLICATION NUMBER: 60/049,728  
; PRIOR FILING DATE: 1997-06-17  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 4621  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (110)..(4318)  
US-09-125-635-9

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Best Local Similarity 79.5%; Pred. No. 3.4;  
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 355 AATAAAGAACAAGGGAAAACTATTTCCAGTGATGATGA 393

## RESULT 5

US-09-445-353E-1  
; Sequence 1, Application US/09445353E  
; Patent No. 6812336  
; GENERAL INFORMATION:  
; APPLICANT: Rosenfeld, Michael G.  
; APPLICANT: Glass, Christopher K.  
; APPLICANT: Rose, David W.  
; APPLICANT: Torchia, Joseph  
; TITLE OF INVENTION: A Transcription Factor Coactivator Protein, p/CIP  
; FILE REFERENCE: 6627-PA1021  
; CURRENT APPLICATION NUMBER: US/09/445,353E  
; CURRENT FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: PCT/US98/12263  
; PRIOR FILING DATE: 1998-06-12  
; PRIOR APPLICATION NUMBER: 60/049,452  
; PRIOR FILING DATE: 1997-06-12  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4860  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (3121)..(3121)  
; OTHER INFORMATION: "n" is any nucleotide  
; NAME/KEY: CDS  
; LOCATION: (110)..(4318)  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS: Joseph Torchia, David W. Rose, Juan Inostroza, Yasutomi Kamei,  
; AUTHORS: Stefan Westin  
; TITLE: The transcriptional co-activator p/CIP binds CBP and mediates  
; TITLE: nuclear receptor function  
; JOURNAL: Nature  
; VOLUME: 387  
; ISSUE: 6634  
; PAGES: 677-684  
; DATE: 1997-06-12  
; DATABASE ACCESSION NUMBER: AF000581  
; DATABASE ENTRY DATE: 1997-06-12  
US-09-445-353E-1

Query Match 52.4%; Score 26.2; DB 3; Length 4860;  
Best Local Similarity 79.5%; Pred. No. 3.5;  
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 355 AATAAAGAACAAGGGAAAACTATTTCCAGTGATGATGA 393



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6	27.8	55.6	6754	7	US-10-159-563-346	Sequence 346, App
7	27.8	55.6	6754	10	US-10-504-173-126	Sequence 126, App
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17	26.4	52.8	403	3	US-09-918-995-3925	Sequence 3925, Ap
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c 19	26.4	52.8	268685	7	US-10-265-071-22	Sequence 22, Appl
c 20	26.4	52.8	268685	7	US-10-025-966A-22	Sequence 22, Appl
c 21	26.4	52.8	268685	10	US-10-933-025-22	Sequence 22, Appl
c 22	26.4	52.8	268685	16	US-11-219-360-22	Sequence 22, Appl
c 23	26.2	52.4	394	8	US-10-424-599-130512	Sequence 130512,
24	26.2	52.4	4621	7	US-10-379-616-9	Sequence 9, Appli
25	26.2	52.4	4860	10	US-10-971-982-1	Sequence 1, Appli
26	25	50.0	35	9	US-10-751-113-1	Sequence 1, Appli
27	24.8	49.6	888	9	US-10-767-795-4182	Sequence 4182, Ap
28	24.8	49.6	1838	8	US-10-424-599-102375	Sequence 102375,
29	24.6	49.2	600	10	US-10-972-079-27987	Sequence 27987, A
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c 31	24.4	48.8	600	10	US-10-972-079-86070	Sequence 86070, A
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c 33	24.4	48.8	171936	7	US-10-265-071-24	Sequence 24, Appl
c 34	24.4	48.8	171936	7	US-10-025-966A-24	Sequence 24, Appl
c 35	24.4	48.8	171936	10	US-10-933-025-24	Sequence 24, Appl
c 36	24.4	48.8	171936	16	US-11-219-360-24	Sequence 24, Appl
37	24.2	48.4	600	10	US-10-972-079-94644	Sequence 94644, A
c 38	23.8	47.6	864	8	US-10-282-122A-24678	Sequence 24678, A
c 39	23.8	47.6	1191	4	US-09-925-065A-27117	Sequence 27117, A
c 40	23.8	47.6	1191	5	US-09-925-065A-27117	Sequence 27117, A
c 41	23.8	47.6	1191	12	US-10-301-480-128354	Sequence 128354,
c 42	23.8	47.6	1191	12	US-10-301-480-741763	Sequence 741763,
c 43	23.8	47.6	10199	8	US-10-398-221-3885	Sequence 3885, Ap
c 44	23.8	47.6	169659	8	US-10-322-696-70	Sequence 70, Appl
45	23.8	47.6	2944528	16	US-11-045-004-1	Sequence 1, Appli

## ALIGNMENTS

## RESULT 1

US-10-751-113-3

; Sequence 3, Application US/10751113

; Publication No. US20040259114A1

; GENERAL INFORMATION:

; APPLICANT: RIEGEL, ANNA T.

; APPLICANT: REITER, RONALD

; APPLICANT: WELLSTEIN, ANTON

; TITLE OF INVENTION: COACTIVATORS IN THE DIAGNOSIS AND TREATMENT OF BREAST

; TITLE OF INVENTION: CANCER

; FILE REFERENCE: 54458-20001.00

; CURRENT APPLICATION NUMBER: US/10/751,113

; CURRENT FILING DATE: 2004-01-05

; PRIOR APPLICATION NUMBER: PCT/US02/21066

; PRIOR FILING DATE: 2002-07-03

; PRIOR APPLICATION NUMBER: 60/302,648

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 3

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-751-113-3

Query Match 100.0%; Score 50; DB 9; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 TGCCATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
        |||||
Db      1 TGCCATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
```

## RESULT 2

US-10-242-535A-57884

; Sequence 57884, Application US/10242535A

; Publication No. US20040013663A1

; GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.

; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis

; FILE REFERENCE: 4231/2005

; CURRENT APPLICATION NUMBER: US/10/242,535A

; CURRENT FILING DATE: 2002-09-12

; PRIOR APPLICATION NUMBER: US 10/085,783

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/275,017

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 57884

; LENGTH: 480

; TYPE: DNA

; ORGANISM: Human

US-10-242-535A-57884

Query Match 55.6%; Score 27.8; DB 8; Length 480;

Best Local Similarity 82.1%; Pred. No. 5.5;

Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
        ||| ||| | |||||
Db      396 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 434
```

## RESULT 3

US-10-085-783A-57884

; Sequence 57884, Application US/10085783A

; Publication No. US20040037841A1

; GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.

; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis

; FILE REFERENCE: 4231/2002

; CURRENT APPLICATION NUMBER: US/10/085,783A

; CURRENT FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/275,017

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 57884

; LENGTH: 480

; TYPE: DNA

; ORGANISM: Human

US-10-085-783A-57884

Query Match 55.6%; Score 27.8; DB 8; Length 480;

Best Local Similarity 82.1%; Pred. No. 5.5;

Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
        ||| ||| | |||||
Db      396 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 434
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RESULT 4

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US-10-414-692-35
; Sequence 35, Application US/10414692
; Publication No. US20030228607A1
; GENERAL INFORMATION:
; APPLICANT: X-Cepto Therapeutics, Inc.
; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic
; TITLE OF INVENTION: profile
; FILE REFERENCE: 8012-002-US
; CURRENT APPLICATION NUMBER: US/10/414,692
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/372,650
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 4263
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-414-692-35
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Query Match 55.6%; Score 27.8; DB 7; Length 4263;  
Best Local Similarity 82.1%; Pred. No. 9.3;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy            12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA    50  
             | | | | | | | | | | | | | | | | | | | | |  
Db          243 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA    281

## RESULT 5

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US-10-388-360-376
; Sequence 376, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffre B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-000IUS
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 6754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-376

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Query Match 55.6%; Score 27.8; DB 7; Length 6754;  
Best Local Similarity 82.1%; Pred. No. 10;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy            12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA     50  
             | | | | | | | | | | | | | | | | | | | | | |  
Db          426 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA     464

## RESULT 6

US-10-159-563-346  
; Sequence 346, Application US/10159563  
; Publication No. US20040009154A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul

```
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 346
; LENGTH: 6754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-346
```

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Query Match          55.6%; Score 27.8; DB 7; Length 6754;
Best Local Similarity 82.1%; Pred. No. 10;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
          | | | | | | | | | | | | | | | | | | | | | |
Db      426 AATAAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 464
```

## RESULT 7

```
US-10-504-173-126
; Sequence 126, Application US/10504173
; Publication No. US20050202428A1
; GENERAL INFORMATION:
; APPLICANT: Axordia Limited
; TITLE OF INVENTION: Pluripotential Stem Cells
; FILE REFERENCE: P101863WO
; CURRENT APPLICATION NUMBER: US/10/504,173
; CURRENT FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 0203359.5
; PRIOR FILING DATE: 2002-02-02
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 6754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-504-173-126
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Query Match          55.6%; Score 27.8; DB 10; Length 6754;
Best Local Similarity 82.1%; Pred. No. 10;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50
          | | | | | | | | | | | | | | | | | | | | | |
Db      426 AATAAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 464
```

## RESULT 8

```
US-10-333-894A-18
; Sequence 18, Application US/10333894A
; Publication No. US20040259085A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Chawnshang
; APPLICANT: Hsing, Ann
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PREDICTING
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: 21108.0001U1
; CURRENT APPLICATION NUMBER: US/10/333,894A
; CURRENT FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6832
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-10-333-894A-18
```

# SCORE Search Results Details for Application 10751113 and Search Result us-10-751-113-3.rnpbn.

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OM nucleic - nucleic search, using sw model

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(without alignments)  
57.324 Million cell updates/sec

Title: US-10-751-113-3  
Perfect score: 50  
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Scoring table: IDENTITY\_NUC  
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Searched: 899801 seqs, 718270062 residues

Total number of hits satisfying chosen parameters: 1799602

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27.8	55.6	7923	8	US-11-283-329-155	Sequence 155, App
2	27.8	55.6	7935	8	US-11-266-748A-56675	Sequence 56675, A
3	27.8	55.6	7935	8	US-11-283-329-153	Sequence 153, App
4	25.2	50.4	789	8	US-11-266-748A-113927	Sequence 113927,
c 5	25.2	50.4	789	8	US-11-266-748A-161615	Sequence 161615,
c 6	22.8	45.6	605	8	US-11-266-748A-80002	Sequence 80002, A
7	22.8	45.6	605	8	US-11-266-748A-132813	Sequence 132813,
8	22.8	45.6	614	8	US-11-266-748A-43663	Sequence 43663, A



	9	22.8	45.6	614	8	US-11-266-748A-209785	Sequence 209785,
	10	22.8	45.6	976	8	US-11-266-748A-354333	Sequence 354333,
c	11	22.8	45.6	976	8	US-11-266-748A-437712	Sequence 437712,
c	12	22.8	45.6	1086	8	US-11-266-748A-75251	Sequence 75251, A
c	13	22.8	45.6	1086	8	US-11-266-748A-108806	Sequence 108806,
	14	22.8	45.6	1086	8	US-11-266-748A-128062	Sequence 128062,
	15	22.8	45.6	2188	8	US-11-266-748A-185432	Sequence 185432,
	16	22.8	45.6	5393	8	US-11-266-748A-22455	Sequence 22455, A
	17	22.8	45.6	5966	8	US-11-266-748A-28012	Sequence 28012, A
c	18	22.6	45.2	1000	8	US-11-266-748A-284293	Sequence 284293,
	19	22.6	45.2	1000	8	US-11-266-748A-335722	Sequence 335722,
c	20	22.6	45.2	1340	6	US-10-953-349-13326	Sequence 13326, A
c	21	22.6	45.2	7011	8	US-11-350-336-9	Sequence 9, Appli
	22	22.4	44.8	1616	8	US-11-266-748A-352261	Sequence 352261,
c	23	22.4	44.8	1616	8	US-11-266-748A-435640	Sequence 435640,
c	24	22.2	44.4	687	8	US-11-266-748A-216355	Sequence 216355,
	25	22.2	44.4	687	8	US-11-266-748A-238191	Sequence 238191,
	26	22.2	44.4	755	8	US-11-266-748A-46670	Sequence 46670, A
	27	22.2	44.4	824	8	US-11-266-748A-163709	Sequence 163709,
	28	22.2	44.4	868	8	US-11-266-748A-14916	Sequence 14916, A
	29	22.2	44.4	1000	8	US-11-266-748A-287318	Sequence 287318,
c	30	22.2	44.4	1000	8	US-11-266-748A-338747	Sequence 338747,
	31	22.2	44.4	1000	8	US-11-266-748A-397979	Sequence 397979,
	32	22.2	44.4	1000	8	US-11-266-748A-404038	Sequence 404038,
c	33	22.2	44.4	1000	8	US-11-266-748A-469025	Sequence 469025,
c	34	22.2	44.4	1000	8	US-11-266-748A-475084	Sequence 475084,
c	35	22.2	44.4	1461	8	US-11-266-748A-192770	Sequence 192770,
c	36	22.2	44.4	1461	8	US-11-266-748A-226616	Sequence 226616,
	37	22.2	44.4	1461	8	US-11-266-748A-240826	Sequence 240826,
	38	22.2	44.4	1701	8	US-11-105-233-2	Sequence 2, Appli
	39	22.2	44.4	1701	8	US-11-105-233-103	Sequence 103, App
	40	22.2	44.4	1916	8	US-11-266-748A-78147	Sequence 78147, A
	41	22.2	44.4	1916	8	US-11-266-748A-110132	Sequence 110132,
c	42	22.2	44.4	1916	8	US-11-266-748A-130958	Sequence 130958,
	43	22.2	44.4	2762	8	US-11-266-748A-31173	Sequence 31173, A
	44	22.2	44.4	3717	8	US-11-266-748A-185976	Sequence 185976,
	45	22.2	44.4	3717	8	US-11-266-748A-193357	Sequence 193357,

## ALIGNMENTS

## RESULT 1

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US-11-283-329-155
; Sequence 155, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 7923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)...(4468)
; OTHER INFORMATION: SRC-3 variant 2
US-11-283-329-155

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Query Match 55.6%; Score 27.8; DB 8; Length 7923;  
Best Local Similarity 82.1%; Pred. No. 0.65;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 448 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 486

```

RESULT 2
US-11-266-748A-56675
; Sequence 56675, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56675
; LENGTH: 7935
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-56675

Query Match          55.6%;  Score 27.8;  DB 8;  Length 7935;
Best Local Similarity 82.1%;  Pred. No. 0.65;
Matches    32;  Conservative    0;  Mismatches    7;  Indels      0;  Gaps      0;

Qy          12 ACTCCAGGACAAGGGAAAAACTATTTCCAATGATGATGA 50
              | | | | | | | | | | | | | | | | | | | |
Db          448 AATAAAAGAGCAAGGAAAAACTATTTCCAATGATGATGA 486

```

### RESULT 3

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US-11-283-329-153
; Sequence 153, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 7935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)...(4480)
; OTHER INFORMATION: SRC-3 variant 1
US-11-283-329-153

Query Match          55.6%;  Score 27.8;  DB 8;  Length 7935;
Best Local Similarity 82.1%;  Pred. No. 0.65;
Matches   32;  Conservative    0;  Mismatches    7;  Indels      0;  Gaps      0;

Qv          12 ACTCCAGGACAAGGGAAAAAATATTTCCAATGATGATGA 50

```

•

US-11-266-748A-113927

; Sequence 113927, Application US/11266748A  
; Publication No. US20060134663A1

Qy 1 TGCCATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATG 46  
 ||||| ||| ||||| || ||| | | |||||  
 Db 440 TGCCATGATGTACGCCAGGCCAAAGGACAAGCCAGGTCGCATGATG 485

US-11-266-748A-161615/c

; Sequence 161615, Application US/11266748A  
; Publication No. US20060134663A1

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; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 161615
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-161615
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Query Match          50.4%; Score 25.2; DB 8; Length 789;
Best Local Similarity 71.7%; Pred. No. 3.5;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

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Qy      1 TGCCATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATG 46
        |||||  ||| |||| ||| ||| || | | ||| |||||
Db      350 TGCCATGATGTACGCCAGGCCAAAGGACAAGCCAGGTCGCATGATG 305
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## RESULT 6

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US-11-266-748A-80002/c
; Sequence 80002, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80002
; LENGTH: 605
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-80002
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Query Match          45.6%; Score 22.8; DB 8; Length 605;
Best Local Similarity 71.4%; Pred. No. 28;
Matches 30; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Qy      5 ATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATG 46
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Db      364 ATATGAGCCTTTAAACATGGGTAAACTAATCCCATTGATG 323
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## RESULT 7

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US-11-266-748A-132813
; Sequence 132813, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
```



4	27.8	55.6	532	9	DB060916	DB060916	DB060916
5	27.8	55.6	537	2	BM146766	BM146766	TCAAP1E73
6	27.8	55.6	545	9	DB071966	DB071966	DB071966
7	27.8	55.6	546	9	DA375387	DA375387	DA375387
8	27.8	55.6	556	9	DB091786	DB091786	DB091786
9	27.8	55.6	557	9	DB134417	DB134417	DB134417
10	27.8	55.6	566	9	DA328439	DA328439	DA328439
11	27.8	55.6	574	9	DB067714	DB067714	DB067714
12	27.8	55.6	581	3	BP351331	BP351331	BP351331
13	27.8	55.6	581	3	BP353869	BP353869	BP353869
14	27.8	55.6	582	3	BP280749	BP280749	BP280749
15	27.8	55.6	583	3	BP282535	BP282535	BP282535
16	27.8	55.6	583	3	BP310850	BP310850	BP310850
17	27.8	55.6	583	3	BP315317	BP315317	BP315317
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19	27.8	55.6	597	9	DA248756	DA248756	DA248756
20	27.8	55.6	609	1	AL698932	AL698932	DKFZp686F
21	27.8	55.6	665	9	DR005834	DR005834	TC116022
22	27.8	55.6	843	5	CD657296	CD657296	AGENCOURT
23	27.6	55.2	908	14	AG891620	AG891620	Oryza sat
24	26.8	53.6	700	7	BB865389	BB865389	BB865389
c 25	26.6	53.2	668	14	DU475651	DU475651	109841573
26	26.4	52.8	718	7	BF270756	BF270756	GA_Eb000
27	26.2	52.4	294	9	DN626023	DN626023	UI-M-EY0-
c 28	26.2	52.4	394	7	AW153178	AW153178	se36h11.y
29	26.2	52.4	443	5	CF165306	CF165306	B0754H03-
30	26.2	52.4	469	8	CN682253	CN682253	E0161G12-
31	26.2	52.4	581	8	CN682136	CN682136	E0160C01-
32	26.2	52.4	637	7	BB659498	BB659498	BB659498
33	26.2	52.4	660	4	BY751007	BY751007	BY751007
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35	26.2	52.4	716	4	CB522550	CB522550	UI-M-GH0-
36	26.2	52.4	1960	6	AK137507	AK137507	Mus muscu
37	26.2	52.4	3923	6	AK156345	AK156345	Mus muscu
38	26.2	52.4	5131	6	AK142306	AK142306	Mus muscu
39	26.2	52.4	5237	6	BC086482	BC086482	Mus muscu
40	26	52.0	424	2	BF887288	BF887288	CM4-TN014
c 41	25.8	51.6	714	7	BB648365	BB648365	BB648365
42	25.8	51.6	721	7	BF215672	BF215672	601881152
43	25.6	51.2	671	10	DV096016	DV096016	327-384-5
44	25.6	51.2	755	7	BE394099	BE394099	601312476
c 45	25.6	51.2	830	14	DX265018	DX265018	OR_ABa015

## ALIGNMENTS

RESULT 1  
CT346760  
LOCUS CT346760 499 bp DNA linear GSS 03-NOV-2005  
DEFINITION Sus scrofa genomic clone CH242-41J6, genomic survey sequence.  
ACCESSION CT346760  
VERSION CT346760.1 GI:79916147  
KEYWORDS GSS.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.  
REFERENCE 1 (bases 1 to 499)  
AUTHORS Humphray, S.J., Plumb, R.W. and Durham, J.L.  
TITLE Direct Submission  
JOURNAL Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquery@sanger.ac.uk Unpublished  
COMMENT This sequence was generated from the SP6 end of BAC 41J6. 41J6 is  
part of the CHORI-242 BAC Library created by P. de Jong. Further  
details: [http://www.sanger.ac.uk/Projects/S\\_scrofa/](http://www.sanger.ac.uk/Projects/S_scrofa/).  
FEATURES  
source 1. .499  
/organism="Sus scrofa"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9823"  
/clone="CH242-41J6"  
/tissue\_type="White blood cells"  
/note="vector pTARBAC1.3\_BamHI"

sex female"

## ORIGIN

Query Match 56.4%; Score 28.2; DB 14; Length 499;  
 Best Local Similarity 80.5%; Pred. No. 31;  
 Matches 33; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 10 ATACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50  
 ||| ||||| || ||||| ||||| ||||| ||||| |||||  
 Db 361 ATAATCCAGGCCATAGGAAAAATATTTCCACTTAAGATGA 401

## RESULT 2

BX643165

LOCUS BX643165 230 bp mRNA linear EST 04-SEP-2003

DEFINITION DKFZp781P1622\_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone  
 DKFZp781P1622 5', mRNA sequence.

ACCESSION BX643165

VERSION BX643165.1 GI:34477498

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 230)

AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,  
 Fobo,G., Han,M. and Wiemann,S.

TITLE EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)

JOURNAL Unpublished (2003)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by BMFZ (Biomedical Research Center at the Heinrich-  
 Heine-University, Duesseldorf/Germany) within the cDNA sequencing  
 consortium of the German Genome Project. No sl sequence available.  
 This clone (DKFZp781P1622) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

source

Location/Qualifiers

1..230

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZp781P1622"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="781 (synonym: hlcc4)"

/note="Vector: pSport1\_Sfi; Site\_1: SfiIA; Site\_2: SfiIB;

cDNA-collection"

## ORIGIN

Query Match 55.6%; Score 27.8; DB 4; Length 230;  
 Best Local Similarity 82.1%; Pred. No. 37;  
 Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50  
 || || || || || ||||| ||||| ||||| ||||| |||||  
 Db 104 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 142

## RESULT 3

DB070018

LOCUS DB070018 531 bp mRNA linear EST 10-DEC-2005

DEFINITION DB070018 TESTI4 Homo sapiens cDNA clone TESTI4012418 5', mRNA  
 sequence.

ACCESSION DB070018

VERSION DB070018.1 GI:83492925

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Query Match	55.6%;	Score 27.8;	DB 9;	Length 531;
Best Local Similarity	82.1%;	Pred. No. 43;		
Matches	32;	Conservative	0;	Mismatches 7;
				Indels 0;
				Gaps 0;

Qy            12 ACTCCAGGACAAGGGAAAACTATTTC CAATGATGATGA       50  
                |     |     |     |     |     |     |     |     |     |     |  
Db           449 AATAAAAGACCAAGGGAAAACTATTTC CAATGATGATGA       487

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RESULT 4
DB060916
LOCUS DB060916 532 bp mRNA linear EST 04-DEC-2005
DEFINITION DB060916 TESTI4 Homo sapiens cDNA clone TESTI4000618 5', mRNA
sequence.
ACCESSION DB060916
VERSION DB060916.1 GI:83255232
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 532)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975

```



Email: [fli-cdna@niftv.com](mailto:fli-cdna@niftv.com)

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES	Location/Qualifiers
source	1..532 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="TESTI4000618" /tissue_type="testis" /clone_lib="TESTI4" /note="Vector: pME18SFL3"

## ORIGIN

Query Match 55.6%; Score 27.8; DB 9; Length 532;  
Best Local Similarity 82.1%; Pred. No. 43;  
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy            12 ACTCCAGGACAAGGGAAAACTATTTCATGATGATGA 50  
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Db           454 AATAAAGAGCAAGGAAAACTATTTCATGATGATGA 492

## RESULT 5

BM146766

LOCUS	BM146766	537 bp	mRNA	linear	EST 30-NOV-2001
-------	----------	--------	------	--------	-----------------

DEFINITION TCAAP1E7316 Pediatric acute myelogenous leukemia cell (FAB M1)  
Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP7316, mRNA  
sequence.

ACCESSION BM146766

VERSION BM146766.1 GI:17165979

KEYWORDS EST.

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 537)

AUTHORS	Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr., Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.
TITLE	Pediatric Leukemia cDNA Sequencing Project (2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@txccc.org  
Seq primer: M13 primer.

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FEATURES
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        Location/Qualifiers
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                /sex="male"
                /tissue_type="leukopheresis"
                /cell_type="myeloid cell"
                /dev_stage="pediatric 6 years"
                /lab_host="DH10B"
                /clone_lib="Pediatric acute myelogenous leukemia cell (FAB
M1) Baylor-HGSC project=TCAA"
                /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCCGAGGAG(T)VN
3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
was primed with a BamH1-dC primer
[5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3'].
Double-stranded cDNA was then digested with BamH1 and XhoI
and directionally cloned into the BamH1 and SalI sites of

```

<http://es.ScoreAccessWeb/GetItem.action?AppId=10751113&seqId=569423&ItemName=...> 8/11/2006

3	27.8	55.6	4263	12	ADJ92834	Adj92834 Human co-
4	27.8	55.6	4495	14	AEC82913	Aec82913 Breast ca
5	27.8	55.6	4789	2	AAX80992	Aax80992 Human ste
6	27.8	55.6	6754	4	AAF26490	Aaf26490 Human SRC
7	27.8	55.6	6754	10	ADK67037	Adk67037 Gene #127
8	27.8	55.6	6754	14	ADY15855	Ady15855 DNA encod
9	27.8	55.6	6754	14	ADY16113	Ady16113 DNA encod
10	27.8	55.6	6754	14	ADY16117	Ady16117 DNA encod
11	27.8	55.6	6832	6	AAD30439	Aad30439 Human amp
12	27.8	55.6	6835	2	AAV99915	Aav99915 AIB1 (Amp
13	27.8	55.6	6835	14	ADY19927	Ady19927 DNA encod
14	27.8	55.6	6835	14	AED18120	Aed18120 Fibrotic
15	27.8	55.6	6845	10	ADE76189	Ade76189 Human AIB
16	27.8	55.6	7088	15	AEF22148	Aef22148 Human bas
17	27.8	55.6	7116	10	ADE53851	Ade53851 Human pro
18	27.8	55.6	7994	14	ADY16115	Ady16115 DNA encod
19	27.8	55.6	8207	10	ADF81691	Adf81691 Leukaemia
20	27.8	55.6	8207	10	ADF81690	Adf81690 Leukaemia
21	27.8	55.6	12414	14	AEA47654	Aea47654 Nucleotid
22	27.6	55.2	34	8	ABX11899	Abx11899 Human AIB
23	26.4	52.8	403	9	ACH16713	Ach16713 Human adu
24	26.4	52.8	86453	14	ADY25730	Ady25730 SULF rela
c 25	26.4	52.8	264965	12	ADN16203	Adn16203 Human sul
c 26	26.4	52.8	268685	6	ABS56563	Abs56563 Human SUL
27	26.2	52.4	4621	2	AAV99919	Aav99919 Murine pC
28	26.2	52.4	4860	2	AAX26000	Aax26000 Murine p/
29	25	50.0	35	8	ABX11898	Abx11898 Human AIB
30	24.8	49.6	888	13	ADR63401	Adr63401 Cotton cD
c 31	24.4	48.8	1179	4	AAK87368	Aak87368 Human imm
32	24.4	48.8	3361	2	AAX80993	Aax80993 Mouse ste
c 33	24.4	48.8	171936	6	ABS56565	Abs56565 Human SUL
c 34	24.4	48.8	171936	12	ADN16205	Adn16205 Mouse sul
c 35	24.2	48.4	1664	4	AAF74192	Aaf74192 DNA encod
c 36	24.2	48.4	110000	14	AEB39174_07	Continuation (8 of
37	24.2	48.4	110000	14	AEB42737_12	Continuation (13 o
c 38	23.8	47.6	864	8	ACA36808	Aca36808 Prokaryot
c 39	23.8	47.6	10199	6	ABQ71072	Abq71072 Listeria
40	23.8	47.6	44528	6	ABA03041_29	Continuation (30 o
c 41	23.8	47.6	169659	12	ADQ59434	Adq59434 Human can
c 42	23.8	47.6	187851	14	ADZ13735	Adz13735 Human can
c 43	23.6	47.2	11614	14	AEA61172	Aea61172 Human HRA
c 44	23.6	47.2	110000	14	AEB42401_22	Continuation (23 o
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## ALIGNMENTS

## RESULT 1

ABX11900

ID ABX11900 standard; cDNA; 50 BP.

XX

AC ABX11900;

XX

DT 16-MAY-2003 (first entry)

XX

DE Human AIB1 delta3 isoform mRNA exon 2/exon 4 junction.

XX

KW Human; ss; exon 2/exon 4 junction; amplified in breast cancer;

KW chromosome 20q; transcription factor; antisense gene therapy; transgenic;

KW siRNA; small inhibitory RNA; cytostatic; intestinal cancer;

KW head and neck cancer; metastatic tissue cancer; neuroblastoma;

KW ovarian cancer; pancreatic cancer; prostate cancer; stomach cancer;

KW breast cancer; AIB1 delta3 isoform.

XX

OS Homo sapiens.

XX

PN WO2003003904-A2.

XX

PD 16-JAN-2003.

XX

PF 03-JUL-2002; 2002WO-US021066.

XX

PR 05-JUL-2001; 2001US-0302648P.

XX

PA (GEOU ) UNIV GEORGETOWN MEDICAL CENT.

XX  
 PI Riegel AT, Reiter R, Wellstein A;  
 XX  
 DR WPI; 2003-221517/21.  
 XX  
 PT New isolated AIB1 isoform as co-activator that potentiates  
 PT transcriptional activity of nuclear hormone receptors, useful for the  
 PT diagnosis, prevention and/or treatment of cancers, in particular breast  
 PT cancer.  
 XX  
 PS Example 6; Fig 9; 47pp; English.  
 XX  
 CC The invention relates to an isolated isoform of an amplified in breast  
 CC cancer 1 (AIB1) transcriptional co-activator. Also included are an  
 CC isolated nucleic sequences that encodes the isoform, a vector that  
 CC contains the nucleic acid, a recombinant cell that contains the nucleic  
 CC acid, a diagnostic kit for the detection of cancer (comprising chemical  
 CC substances that are specifically reactive to the AIB1 isoform or the  
 CC nucleic acid), an anti-AIB1 isoform antibody (or antibody fragment),  
 CC detection of cancer in a patient (comprising contacting a biological  
 CC sample obtained from the patient with at least one chemical substance  
 CC that specifically binds to the AIB1 isoform or the nucleic acid, and  
 CC detecting binding), a pharmaceutical composition (comprising an agent  
 CC that specifically binds to the AIB1 isoform, and prevents a co-activation  
 CC of a transcription factor when administered to a patient), an siRNA  
 CC (small inhibitory RNA) that inhibits expression of a transcriptional co-  
 CC activator protein, a transgenic animal comprising a recombinant gene that  
 CC encodes the AIB1 isoform and creating the transgenic animal. The  
 CC compositions comprising the AIB1 isoform or nucleic acids that bind to  
 CC the AIB1 isoform, are useful for the diagnosis, prevention and/or  
 CC treatment of disorders associated with the co-activator isoforms, such as  
 CC cancers of the intestines, head and neck, metastatic tissue,  
 CC neuroblastoma, ovaries, pancreas, prostate, stomach, and in particular  
 CC cancer of the breast. The gene for AIB1 is located on chromosome 20q. The  
 CC present sequence is the junction region of the AIB1 delta3 isoform mRNA  
 CC for exons 2 and 4 (unique to the delta3 isoform), which was targeted by  
 CC an siRNA  
 XX  
 SQ Sequence 50 BP; 18 A; 9 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 8; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 3e-09;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCCATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50  
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 Db 1 TGCCATGTGATACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50

## RESULT 2

ADV43475

ID ADV43475 standard; cDNA; 4239 BP.

XX

AC ADV43475;

XX

DT 10-MAR-2005 (first entry)

XX

DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1103.

XX

KW microarray; psychoneuroendocrinimmune; chronic fatigue;

KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;

KW cancer; neoplasm; infection; expressed sequence tag; ss.

XX

OS Homo sapiens.

XX

PN WO2004108899-A2.

XX

PD 16-DEC-2004.

XX

PF 04-JUN-2004; 2004WO-US017686.

XX

PR 04-JUN-2003; 2003US-0475915P.

XX

PA (USSH ) US DEPT HEALTH &amp; HUMAN SERVICES.

XX

PI Nicholson A, Vernon SD;

Qy            12 ACTCCAGGACAAGGGAAAACTATTTCCAATGATGATGA 50  
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Db           243 AATAAAGAGCAAGGAAAACTATTTCCAATGATGATGA 281

